



IFW16

RAW SEQUENCE LISTING

DATE: 12/23/2004

PATENT APPLICATION: US/09/725,019A

TIME: 14:34:23

Input Set : N:\Crf3\RULE60\09725019a.raw.txt

Output Set: N:\CRF4\12232004\I725019A.raw

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1 <110> APPLICANT: Thompson, John E.
2   Wang, Tzann-Wei
3   Lu, Dongen Lilly
4 <120> TITLE OF INVENTION: DNA ENCODING A PLANT DEOXYHYPUSINE SYNTHASE, TRANSGENIC
5   PLANTS AND A METHOD FOR CONTROLLING PROGRAMMED CELL
6   DEATH IN PLANTS
7 <130> FILE REFERENCE: 10799/9
8 <140> CURRENT APPLICATION NUMBER: US/09/725,019A
9 <141> CURRENT FILING DATE: 2000-11-29
10 <150> PRIOR APPLICATION NUMBER: US/09/597,771
11 <151> PRIOR FILING DATE: 2000-06-19
12 <150> PRIOR APPLICATION NUMBER: 09/348,675
13 <151> PRIOR FILING DATE: 1999-07-06
14 <160> NUMBER OF SEQ ID NOS: 35
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1609
19 <212> TYPE: DNA
20 <213> ORGANISM: Lycopersicon sp.
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (54..1196)
24 <220> FEATURE:
25 <223> OTHER INFORMATION: DHS
26 <400> SEQUENCE: 1
27   cgcagaaact cgcggcgga gtcttggtcc ctacataatc ttggtctgca ata atg           56
28                                     Met
29                                     1
30   gga gaa gct ctg aag tac agt atc atg gac tca gta aga tcg gta gtt           104
31   Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val Val
32               5                      10                      15
33   ttc aaa gaa tcc gaa aat cta gaa ggt tct tgc act aaa atc gag ggc           152
34   Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu Gly
35               20                      25                      30
36   tac gac ttc aat aaa ggc gtt aac tat gct gag ctg atc aag tcc atg           200
37   Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser Met
38               35                      40                      45
39   gtt tcc act ggt ttc caa gca tct aat ctt ggt gac gcc att gca att           248
40   Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala Ile
41               50                      55                      60                      65
42   gtt aat caa atg cta gat tgg agg ctt tca cat gag ctg ccc acg gag           296
43   Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr Glu
44               70                      75                      80

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45	gat tgc agt gaa gaa gaa aga gat gtt gca tac aga gag tcg gta acc	344
46	Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val Thr	
47	85 90 95	
48	tgc aaa atc ttc ttg ggg ttc act tca aac ctt gtt tct tct ggt gtt	392
49	Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val	
50	100 105 110	
51	aga gac act gtc cgc tac ctt gtt cag cac cgg atg gtt gat gtt gtg	440
52	Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val Val	
53	115 120 125	
54	ggt act aca gct ggt ggt att gaa gag gat ctc ata aag tgc ctc gca	488
55	Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu Ala	
56	130 135 140 145	
57	cca acc tac aag ggg gac ttc tct tta cct gga gct tct cta cga tcg	536
58	Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg Ser	
59	150 155 160	
60	aaa gga ttg aac cgt att ggt aac tta ttg gtt cct aat gac aac tac	584
61	Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr	
62	165 170 175	
63	tgc aaa ttt gag aat tgg atc atc cca gtt ttt gac caa atg tat gag	632
64	Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr Glu	
65	180 185 190	
66	gag cag att aat gag aag gtt cta tgg aca cca tct aaa gtc att gct	680
67	Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile Ala	
68	195 200 205	
69	cgt ctg ggt aaa gaa att aat gat gaa acc tca tac ttg tat tgg gct	728
70	Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp Ala	
71	210 215 220 225	
72	tac aag aac cgg att cct gtc ttc tgt cct ggc ttg acg gat gga tca	776
73	Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser	
74	230 235 240	
75	ctt ggt gac atg cta tac ttc cat tct ttc aaa aag ggt gat cca gat	824
76	Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro Asp	
77	245 250 255	
78	aat cca gat ctt aat cct ggt cta gtc ata gac att gta gga gat att	872
79	Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp Ile	
80	260 265 270	
81	agg gcc atg aat ggt gaa gct gtc cat gct ggt ttg agg aag aca gga	920
82	Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr Gly	
83	275 280 285	
84	atg att ata ctg ggt gga ggg ctg cct aag cac cat gtt tgc aat gcc	968
85	Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn Ala	
86	290 295 300 305	
87	aat atg atg cgc aat ggt gca gat ttt gcc gtc ttc att aac acc gca	1016
88	Asn Met Met Arg Gly Ala Asp Phe Ala Val Phe Ile Asn Thr Ala	
89	310 315 320	
90	caa gag ttt gat ggt agt gac tct ggt gcc cgt cct gat gaa gct gta	1064
91	Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val	
92	325 330 335	
93	tca tgg gga aag ata cgt ggt ggt gcc aag act gtg aag gtg cat tgt	1112

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```

94      Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His Cys
95              340                      345                      350
96      gat gca acc att gca ttt ccc ata tta gta gct gag aca ttt gca gct      1160
97      Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala Ala
98              355                      360                      365
99      aag agt aag gaa ttc tcc cag ata agg tgc caa gtt tgaacattga      1206
100     Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
101             370                      375                      380
102     ggaagctgtc cttccgacca cacatatgaa ttgctagctt ttgaagccaa cttgctagtg      1266
103     tgcagcacca tttattctgc aaaactgact agagagcagg gtatattcct ctaccccgag      1326
104     ttagacgaca tcctgtatgg ttcaaattaa ttatttttct ccccttcaca ccattgttatt      1386
105     tagttctctt cctcttcgaa agtgaagagc ttagatgttc atagggttttg aattatgttg      1446
106     gaggttggtg ataactgact agtctcttta ccatatagat aatgtatcct tgtactatga      1506
107     gattttgggt gtgtttgata ccaaggaaaa tgtttatttg gaaaacaatt ggatttttaa      1566
108     tttatttttt cttgttttaa aaaaaaaaaa aaaaaaaaaa aaa      1609
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 381
112 <212> TYPE: PRT
113 <213> ORGANISM: Lycopersicon sp.
114 <220> FEATURE:
115 <223> OTHER INFORMATION: DHS
116 <400> SEQUENCE: 2
117     Met Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val
118         1             5             10             15
119     Val Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu
120             20             25             30
121     Gly Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser
122             35             40             45
123     Met Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala
124             50             55             60
125     Ile Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr
126             65             70             75             80
127     Glu Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val
128             85             90             95
129     Thr Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly
130             100            105            110
131     Val Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val
132             115            120            125
133     Val Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu
134             130            135            140
135     Ala Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg
136             145            150            155            160
137     Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn
138             165            170            175
139     Tyr Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr
140             180            185            190
141     Glu Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile
142             195            200            205
143     Ala Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp

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144          210          215          220
145 Ala Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly
146 225          230          235          240
147 Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro
148          245          250          255
149 Asp Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp
150          260          265          270
151 Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr
152          275          280          285
153 Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn
154 290          295          300
155 Ala Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr
156 305          310          315          320
157 Ala Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala
158          325          330          335
159 Val Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His
160          340          345          350
161 Cys Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala
162          355          360          365
163 Ala Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
164          370          375          380
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 24
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
172 <400> SEQUENCE: 3
173 agtctagaag gtgctcgccc tgat 24
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 34
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
181 <400> SEQUENCE: 4
182 gactgcagtc gacatcgatt tttttttttt tttt 34
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 2272
186 <212> TYPE: DNA
187 <213> ORGANISM: Arabidopsis sp.
188 <220> FEATURE:
189 <221> NAME/KEY: CDS
190 <222> LOCATION: (68..265, 348..536, 624..842, 979..1065,
191 1154..1258, 1575..1862)
192 <400> SEQUENCE: 5
193 gaactcccaa aacctctac tactacactt tcagatccaa ggaaatcaat tttgtcattc 60
194 gagcaac atg gag gat gat cgt gtt ttc tct tcg gtt cac tca aca gtt 109
195 Met Glu Asp Asp Arg Val Phe Ser Ser Val His Ser Thr Val

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196          1          5          10
197 ttc aaa gaa tcc gaa tca ttg gaa gga aag tgt gat aaa atc gaa gga 157
198 Phe Lys Glu Ser Glu Ser Leu Glu Gly Lys Cys Asp Lys Ile Glu Gly
199 15          20          25          30
200 tac gat ttc aat caa gga gta gat tac cca aag ctt atg cga tcc atg 205
201 Tyr Asp Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met
202          35          40          45
203 ctc acc acc gga ttt caa gcc tcg aat ctc ggc gaa gct att gat gtc 253
204 Leu Thr Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val
205          50          55          60
206 gtc aat caa atg gttcgtttct cgaattcatc aaaaataaaa attccttctt 305
207 Val Asn Gln Met
208          65
209 tttgttttcc tttgttttgg gtgaattagt aatgacaaag ag ttt gaa ttt gta 359
210          Phe Glu Phe Val
211          70
212 ttg aag cta gat tgg aga ctg gct gat gaa act aca gta gct gaa gac 407
213 Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu Thr Thr Val Ala Glu Asp
214          75          80          85
215 tgt agt gaa gag gag aag aat cca tcg ttt aga gag tct gtc aag tgt 455
216 Cys Ser Glu Glu Glu Lys Asn Pro Ser Phe Arg Glu Ser Val Lys Cys
217          90          95          100
218 aaa atc ttt cta ggt ttc act tca aat ctt gtt tca tct ggt gtt aga 503
219 Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val Arg
220          105          110          115
221 gat act att cgt tat ctt gtt cag cat cat atg gtttgtgatt tttgctttat 556
222 Asp Thr Ile Arg Tyr Leu Val Gln His His Met
223          120          125
224 caccctgctt ttttatagat gttaaaattt tcgagcttta gttttgattt caatggtttt 616
225 tctgcag gtt gat gtt ata gtc acg aca act ggt ggt gtt gag gaa gat 665
226 Val Asp Val Ile Val Thr Thr Thr Gly Gly Val Glu Glu Asp
227          130          135          140
228 ctc ata aaa tgc ctt gca cct aca ttt aaa ggt gat ttc tct cta cct 713
229 Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ser Leu Pro
230          145          150          155
231 gga gct tat tta agg tca aag gga ttg aac cga att ggg aat ttg ctg 761
232 Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu
233          160          165          170          175
234 gtt cct aat gat aac tac tgc aag ttt gag gat tgg atc att ccc atc 809
235 Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile
236          180          185          190
237 ttt gac gag atg ttg aag gaa cag aaa gaa gag gtattgcttt atctttcctt 862
238 Phe Asp Glu Met Leu Lys Glu Gln Lys Glu Glu
239          195          200
240 tttatatgat ttgagatgat tctgtttgtg cgtcactagt ggagatagat tttgattcct 922
241 ctcttgcatc attgacttcg ttggtgaatc cttctttctc tggtttttcc ttgtag 978
242 aat gtg ttg tgg act cct tct aaa ctg tta gca cgg ctg gga aaa gaa 1026
243 Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu
244          205          210          215

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/23/2004
PATENT APPLICATION: US/09/725,019A TIME: 14:34:24

Input Set : N:\Crf3\RULE60\09725019a.raw.txt
Output Set: N:\CRF4\12232004\I725019A.raw

Please Note:

Presence of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

q#:19; N Pos. 6
q#:31; N Pos. 542

Valid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

q#:1; Line(s) 4

VARIABLE LOCATION SUMMARY

DATE: 12/23/2004

PATENT APPLICATION: US/09/725,019A

TIME: 14:34:24

Input Set : N:\Crf3\RULE60\09725019a.raw.txt

Output Set: N:\CRF4\12232004\I725019A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:19; N Pos. 6

Seq#:31; N Pos. 542

VERIFICATION SUMMARY

DATE: 12/23/2004

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Input Set : N:\Crf3\RULE60\09725019a.raw.txt

Output Set: N:\CRF4\12232004\I725019A.raw

L:764 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:19

L:764 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:19

L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0

L:986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:496



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1	CRFE	10

Total number of pages: 10

Remarks:

Order of re-scan issued on